RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/538,902_

Source: _PCT_

Date Processed by STIC: _06-22-2005_

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PCT

RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: US/10/538,902   TIME: 10:32:46

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538902.raw**

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   3 <110> APPLICANT: University of Medicine and Dentistry of New Jersey
   4        Kaplan, Jeffrey B.
   6 <120> TITLE OF INVENTION: Compositions and Methods for Enzymatic Detachment of
Bacterial and Fungal
   7        Biofilms
   9 <130> FILE REFERENCE: UMD-0015
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/538,902
C--> 11 <141> CURRENT FILING DATE: 2005-06-14
   11 <150> PRIOR APPLICATION NUMBER: US 60/435,817
   12 <151> PRIOR FILING DATE: 2002-12-20
   14 <160> NUMBER OF SEQ ID NOS: 15
   16 <170> SOFTWARE: PatentIn version 3.1
   18 <210> SEQ ID NO: 1
   19 <211> LENGTH: 1146
   20 <212> TYPE: DNA
   21 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
   23 <400> SEQUENCE: 1
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   26 aattgttgcg taaaaggcaa ttccatatat ccgcaaaaaa caagtaccaa gcagaccgga     120
   28 ttaatgctgg acatcgcccg acatttttat tcacccgagg tgattaaatc ctttattgat     180
   30 accatcagcc tttccggcgg taattttctg cacctgcatt tttccgacca tgaaaactat     240
   32 gcgatagaaa gccatttact taatcaacgt gcggaaaatg ccgtgcaggg caaagacggt     300
   34 atttatatta atccttatac cggaaagcca ttcttgagtt atcggcaact tgacgatatc     360
   36 aaagcctatg ctaaggcaaa aggcattgag ttgattcccg aacttgacag cccgaatcac     420
   38 atgacggcga tctttaaact ggtgcaaaaa gacagagggg tcaagtacct tcaaggatta     480
   40 aaatcacgcc aggtagatga tgaaattgat attactaatg ctgacagtat tactttttatg     540
   42 caatctttaa tgagtgaggt tattgatatt tttggcgaca cgagtcagca ttttcatatt     600
   44 ggtggcgatg aatttggtta ttctgtggaa agtaatcatg agtttattac gtatgccaat     660
   46 aaactatcct acttttttaga gaaaaaaggg ttgaaaccc gaatgtggaa tgacggatta     720
   48 attaaaaata cttttgagca aatcaacccg aatattgaaa ttacttattg gagctatgat     780
   50 ggcgatacgc aggacaaaaa tgaagctgcc gagcgccgtg atatgcgggt cagtttgccg     840
   52 gagttgctgg cgaaaggctt tactgtcctg aactataatt cctattatct ttacattgtt     900
   54 ccgaaagctt caccaacctt ctcgcaagat gccgcctttg ccgccaaaga tgttataaaa     960
   56 aattgggatc ttggtgtttg ggatggacga aacaccaaaa accgcgtaca aaatactcat    1020
   58 gaaatagccg gcgcagcatt atcgatctgg ggagaagatg caaaagcgct gaaagacgaa    1080
   60 acaattcaga aaaacacgaa aagtttattg gaagcggtga ttcataagac gaatggggat    1140
   62 gagtga                                                            1146
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   66 <211> LENGTH: 381
   67 <212> TYPE: PRT
   68 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain CU1000N
   70 <400> SEQUENCE: 2
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   73 1               5                   10                  15
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 76 Phe Ser Val Leu Asn Cys Cys Val Lys Gly Asn Ser Ile Tyr Pro Gln
 77         20                  25                  30
 80 Lys Thr Ser Thr Lys Gln Thr Gly Leu Met Leu Asp Ile Ala Arg His
 81         35                  40                  45
 84 Phe Tyr Ser Pro Glu Val Ile Lys Ser Phe Ile Asp Thr Ile Ser Leu
 85     50                  55                  60
 88 Ser Gly Gly Asn Phe Leu His Leu His Phe Ser Asp His Glu Asn Tyr
 89 65                  70                  75                  80
 92 Ala Ile Glu Ser His Leu Leu Asn Gln Arg Ala Glu Asn Ala Val Gln
 93                 85                  90                  95
 96 Gly Lys Asp Gly Ile Tyr Ile Asn Pro Tyr Thr Gly Lys Pro Phe Leu
 97             100                 105                 110
100 Ser Tyr Arg Gln Leu Asp Asp Ile Lys Ala Tyr Ala Lys Ala Lys Gly
101         115                 120                 125
104 Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn His Met Thr Ala Ile
105     130                 135                 140
108 Phe Lys Leu Val Gln Lys Asp Arg Gly Val Lys Tyr Leu Gln Gly Leu
109 145                 150                 155                 160
112 Lys Ser Arg Gln Val Asp Asp Glu Ile Asp Ile Thr Asn Ala Asp Ser
113             165                 170                 175
116 Ile Thr Phe Met Gln Ser Leu Met Ser Glu Val Ile Asp Ile Phe Gly
117         180                 185                 190
120 Asp Thr Ser Gln His Phe His Ile Gly Gly Asp Glu Phe Gly Tyr Ser
121         195                 200                 205
124 Val Glu Ser Asn His Glu Phe Ile Thr Tyr Ala Asn Lys Leu Ser Tyr
125     210                 215                 220
128 Phe Leu Glu Lys Lys Gly Leu Lys Thr Arg Met Trp Asn Asp Gly Leu
129 225                 230                 235                 240
132 Ile Lys Asn Thr Phe Glu Gln Ile Asn Pro Asn Ile Glu Ile Thr Tyr
133             245                 250                 255
136 Trp Ser Tyr Asp Gly Asp Thr Gln Asp Lys Asn Glu Ala Ala Glu Arg
137         260                 265                 270
140 Arg Asp Met Arg Val Ser Leu Pro Glu Leu Leu Ala Lys Gly Phe Thr
141         275                 280                 285
144 Val Leu Asn Tyr Asn Ser Tyr Tyr Leu Tyr Ile Val Pro Lys Ala Ser
145     290                 295                 300
148 Pro Thr Phe Ser Gln Asp Ala Ala Phe Ala Ala Lys Asp Val Ile Lys
149 305                 310                 315                 320
152 Asn Trp Asp Leu Gly Val Trp Asp Gly Arg Asn Thr Lys Asn Arg Val
153             325                 330                 335
156 Gln Asn Thr His Glu Ile Ala Gly Ala Ala Leu Ser Ile Trp Gly Glu
157         340                 345                 350
160 Asp Ala Lys Ala Leu Lys Asp Glu Thr Ile Gln Lys Asn Thr Lys Ser
161         355                 360                 365
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165     370                 375                 380
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 555
170 <212> TYPE: DNA
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176 gagaaaacg  gaacctattt caatccgaaa acaaataagc cgtttctcac ttataaacag   120
178 ctcaatgaaa ttatctatta tgccaaagaa cgaaatattg aaattgtgcc tgaagtcgat   180
180 agcccgaatc atatgacggc gattttgat  cttttaaccc ttaagcacgg taaggagtat   240
182 gtgaaagggc tgaaatcgcc ttatcttgcc gaggaaatcg atattaataa ccctgaagcg   300
184 gttgaaatta tcaaaacctt aatcggtgaa gtgatttata tttttgggca ttccagccga   360
186 cactttcata tcggcggaga cgaatttagt tatgcggtcg aaaacaatca cgaatttatt   420
188 cgttatgtaa atacgctaaa tgactttatt aataacaaag gactaattac ccgtatttgg   480
190 aacgacggtt tgattaaaaa caatttaaat gagcttaatc ggaatatcga aattacttat   540
192 tggagctacg acggt                                                    555
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 185
197 <212> TYPE: PRT
198 <213> ORGANISM: Actinobacillus ligniersii strain 19393
200 <400> SEQUENCE: 4
202 Asp His Glu Asn Tyr Ala Leu Glu Ser Ser Tyr Leu Glu Gln Arg Glu
203 1               5                   10                  15
206 Glu Asn Ala Val Glu Lys Asn Gly Thr Tyr Phe Asn Pro Lys Thr Asn
207             20                  25                  30
210 Lys Pro Phe Leu Thr Tyr Lys Gln Leu Asn Glu Ile Ile Tyr Tyr Ala
211         35                  40                  45
214 Lys Glu Arg Asn Ile Glu Ile Val Pro Glu Val Asp Ser Pro Asn His
215     50                  55                  60
218 Met Thr Ala Ile Phe Asp Leu Leu Thr Leu Lys His Gly Lys Glu Tyr
219 65                  70                  75                  80
222 Val Lys Gly Leu Lys Ser Pro Tyr Leu Ala Glu Glu Ile Asp Ile Asn
223             85                  90                  95
226 Asn Pro Glu Ala Val Glu Ile Ile Lys Thr Leu Ile Gly Glu Val Ile
227             100                 105                 110
230 Tyr Ile Phe Gly His Ser Ser Arg His Phe His Ile Gly Gly Asp Glu
231         115                 120                 125
234 Phe Ser Tyr Ala Val Glu Asn Asn His Glu Phe Ile Arg Tyr Val Asn
235     130                 135                 140
238 Thr Leu Asn Asp Phe Ile Asn Asn Lys Gly Leu Ile Thr Arg Ile Trp
239 145                 150                 155                 160
242 Asn Asp Gly Leu Ile Lys Asn Asn Leu Asn Glu Leu Asn Arg Asn Ile
243             165                 170                 175
246 Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
247             180                 185
250 <210> SEQ ID NO: 5
251 <211> LENGTH: 558
252 <212> TYPE: DNA
253 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain IDH781
255 <400> SEQUENCE: 5
256 gatcatgaaa actatgcgat agaaagccat ttacttaatc aacgtgcgga aaatgccgta    60
258 cagggcaaag acggtattta tattaatcct tataccggaa agccattctt gagttatcga   120
260 caacttgacg atatcaaagc ctatgctaag gcaaaaggca ttgagttgat tcccgaactt   180
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262 gatagtccga atcacatgac ggcgatcttt aaactggtgc aaaaagacag agggatcaag   240
264 tatcttcaag gattaaaatc acgccaggta gatgatgaaa ttgatattac taatgctgac   300
266 agtattgctt ttatgcaatc tttaatgagt gaggttattg atattttttgg cgacacgagt   360
268 cagcattttc atattggtgg cgatgaattt ggttattctg tggaaagtaa tcatgagttt   420
270 attacgtatg ccaataaact atcctacttt ttagagaaaa aggggttgaa aacccgaatg   480
272 tggaatgacg gattaattaa aagtactttt gagcaaatca acccgaatat tgaaattact   540
274 tattggagct atgatggc                                                 558
277 <210> SEQ ID NO: 6
278 <211> LENGTH: 186
279 <212> TYPE: PRT
280 <213> ORGANISM: Actinobacillus actinomycetemcomitans strain IDH781
282 <400> SEQUENCE: 6
284 Asp His Glu Asn Tyr Ala Ile Glu Ser His Leu Leu Asn Gln Arg Ala
285 1               5                   10                  15
288 Glu Asn Ala Val Gln Gly Lys Asp Gly Ile Tyr Ile Asn Pro Tyr Thr
289             20                  25                  30
292 Gly Lys Pro Phe Leu Ser Tyr Arg Gln Leu Asp Asp Ile Lys Ala Tyr
293         35                  40                  45
296 Ala Lys Ala Lys Gly Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn
297     50                  55                  60
300 His Met Thr Ala Ile Phe Lys Leu Val Gln Lys Asp Arg Gly Ile Lys
301 65                  70                  75                  80
304 Tyr Leu Gln Gly Leu Lys Ser Arg Gln Val Asp Asp Glu Ile Asp Ile
305             85                  90                  95
308 Thr Asn Ala Asp Ser Ile Ala Phe Met Gln Ser Leu Met Ser Glu Val
309             100                 105                 110
312 Ile Asp Ile Phe Gly Asp Thr Ser Gln His Phe His Ile Gly Gly Asp
313         115                 120                 125
316 Glu Phe Gly Tyr Ser Val Glu Ser Asn His Glu Phe Ile Thr Tyr Ala
317     130                 135                 140
320 Asn Lys Leu Ser Tyr Phe Leu Glu Lys Lys Gly Leu Lys Thr Arg Met
321 145                 150                 155                 160
324 Trp Asn Asp Gly Leu Ile Lys Ser Thr Phe Glu Gln Ile Asn Pro Asn
325                 165                 170                 175
328 Ile Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
329             180                 185
332 <210> SEQ ID NO: 7
333 <211> LENGTH: 558
334 <212> TYPE: DNA
335 <213> ORGANISM: Haemophilus aphrophilus strain NJ8700
337 <400> SEQUENCE: 7
338 gaccacgaaa attatgcttt agaaagcagg ttgttgaatc agcgggcaga aaacgcaatt   60
340 ttaaataaaa acggaattta tattaatcct tacaccaata agcctttctt gagttatcaa   120
342 cagttggatg acattaaagc atatgcaaaa ttaaaaggta ttgagcttat cccgaatta   180
344 gatagcccga atcacatgac agcgattttt accttattaa aaaaagaaaa aggaaaaaat   240
346 tatcttcaat cgttaaaatc accacaaaat gatgaggaaa ttagcattac caatccggac   300
348 agcattgcat ttatgcaatc cttattaaca gaggtaattc ataccttttgg cgatagcacc   360
350 aagcattttc atattggcgg agatgagttt ggttatgatg aaaatagtaa tcatgaattt   420
352 attacctatg ccaataaatt ggctgatttt ttaagagaaa aaggattaaa aactcgaatt   480
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354 tggaatgatg gtttaattaa aaataccata gatcaattaa atcctaatat tgaaattacc   540
356 tactggagtt acgacggc                                                 558
359 <210> SEQ ID NO: 8
360 <211> LENGTH: 186
361 <212> TYPE: PRT
362 <213> ORGANISM: Haemophilus aphrophilus strain NJ8700
364 <400> SEQUENCE: 8
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367 1               5                   10                  15
370 Glu Asn Ala Ile Leu Asn Lys Asn Gly Ile Tyr Ile Asn Pro Tyr Thr
371             20                  25                  30
374 Asn Lys Pro Phe Leu Ser Tyr Gln Gln Leu Asp Asp Ile Lys Ala Tyr
375         35                  40                  45
378 Ala Lys Leu Lys Gly Ile Glu Leu Ile Pro Glu Leu Asp Ser Pro Asn
379     50                  55                  60
382 His Met Thr Ala Ile Phe Thr Leu Leu Lys Lys Glu Lys Gly Lys Asn
383 65                  70                  75                  80
386 Tyr Leu Gln Ser Leu Lys Ser Pro Gln Asn Asp Glu Glu Ile Ser Ile
387                 85                  90                  95
390 Thr Asn Pro Asp Ser Ile Ala Phe Met Gln Ser Leu Leu Thr Glu Val
391             100                 105                 110
394 Ile His Thr Phe Gly Asp Ser Thr Lys His Phe His Ile Gly Gly Asp
395         115                 120                 125
398 Glu Phe Gly Tyr Asp Glu Asn Ser Asn His Glu Phe Ile Thr Tyr Ala
399     130                 135                 140
402 Asn Lys Leu Ala Asp Phe Leu Arg Glu Lys Gly Leu Lys Thr Arg Ile
403 145                 150                 155                 160
406 Trp Asn Asp Gly Leu Ile Lys Asn Thr Ile Asp Gln Leu Asn Pro Asn
407                 165                 170                 175
410 Ile Glu Ile Thr Tyr Trp Ser Tyr Asp Gly
411                 180                 185
414 <210> SEQ ID NO: 9
415 <211> LENGTH: 555
416 <212> TYPE: DNA
417 <213> ORGANISM: Actinobacillus pleuropneumoniae strain IA5
419 <400> SEQUENCE: 9
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422 gagaaaaacg gaacctattt caatccgaaa acaaataagc cgtttctcac ttataaacag   120
424 ctcaatgaaa ttatctatta tgccaaagaa cgaaatattg aaattgtgcc tgaagtcgat   180
426 agcccgaatc atatgacggc gattttgat cttttaaccc ttaagcacgg aaaggaatac    240
428 gtaaaagggc taaatcgcc ttatatcgcc gaggaaatcg atattaataa ccccgaagcg    300
430 gttgaagtta ttaaaacctt aatcggtgaa gtgatctata ttttcggaca ttcaagccgg   360
432 catttccata tcggcggaga tgaatttagc tatgcggtcg aaaataatca tgaatttatt   420
434 cggtatgtga ataccttaaa tgattttatc aattccaaag gctaattac ccgtgtttgg    480
436 aatgacggtt tgatcaaaaa caacttaagc gaactcaata aaaacattga aatcacttac   540
438 tggagctacg acggt                                                    555
441 <210> SEQ ID NO: 10
442 <211> LENGTH: 185
443 <212> TYPE: PRT
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/22/2005
PATENT APPLICATION: US/10/538,902   TIME: 10:32:48

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538902.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 1
Seq#:13; N Pos. 3

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY   DATE: 06/22/2005
PATENT APPLICATION: **US/10/538,902**   TIME: 10:32:48

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06222005\J538902.raw**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
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